

SEQUENCE LISTING

<110> Gosling, Jennifa
Dairaghi, Daniel J.
Hanley, Michael
Miao, Zhenhua
Talbot, Dale
Schall, Thomas J.
ChemoCentryx, Inc.

<120> Chemokine Receptor

<130> 019934-0007210US

<140> US 09/721,495

<141> 2000-11-21

<150> US 60/159,015

<151> 1999-10-12

<150> US 60/159,210

<151> 1999-10-13

<150> US 60/172,979

<151> 1999-12-20

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<151> 1999-12-28

<150> US 60/186,626

<151> 2000-03-03

<150> US 09/686,019

<151> 2000-10-10

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<170> PatentIn Ver. 2.1

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<211> 1147

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (1)..(1053)

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<223> chemokine receptor CCX CKR

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gaa atg aat ggc act tat gac tac agt caa tat gaa ctg atc tgt atc	96
Glu Met Asn Gly Thr Tyr Asp Tyr Ser Gln Tyr Glu Leu Ile Cys Ile	
20 25 30	

aaa gaa gat gtc aga gaa ttt gca aaa gtt ttc ctc cct gta ttc ctc	144
Lys Glu Asp Val Arg Glu Phe Ala Lys Val Phe Leu Pro Val Phe Leu	
35 40 45	
aca ata gtt ttc gtc att gga ctt gca ggc aat tcc atg gta gtg gca	192
Thr Ile Val Phe Val Ile Gly Leu Ala Gly Asn Ser Met Val Val Ala	
50 55 60	
att tat gcc tat tac aag aaa cag aga acc aaa aca gat gtg tac atc	240
Ile Tyr Ala Tyr Tyr Lys Lys Gln Arg Thr Lys Thr Asp Val Tyr Ile	
65 70 75 80	
ctg aat ttg gct gta gca gat tta ctc ctt cta ttc act ctg cct ttt	288
Leu Asn Leu Ala Val Ala Asp Leu Leu Leu Leu Phe Thr Leu Pro Phe	
85 90 95	
tgg gct gtt aat gca gtt cat ggg tgg gtt tta ggg aaa ata atg tgc	336
Trp Ala Val Asn Ala Val His Gly Trp Val Leu Gly Lys Ile Met Cys	
100 105 110	
aaa ata act tca gcc ttg tac aca cta aac ttt gtc tct gga atg cag	384
Lys Ile Thr Ser Ala Leu Tyr Thr Leu Asn Phe Val Ser Gly Met Gln	
115 120 125	
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Phe Leu Ala Cys Ile Ser Ile Asp Arg Tyr Val Ala Val Thr Lys Val	
130 135 140	
ccc agc caa tca gga gtg gga aaa cca tgc tgg atc atc tgt ttc tgt	480
Pro Ser Gln Ser Gly Val Gly Lys Pro Cys Trp Ile Ile Cys Phe Cys	
145 150 155 160	
gtc tgg atg gct gcc atc ttg ctg agc ata ccc cag ctg gtt ttt tat	528
Val Trp Met Ala Ala Ile Leu Leu Ser Ile Pro Gln Leu Val Phe Tyr	
165 170 175	
aca gta aat gac aat gct agg tgc att ccc att ttc ccc cgc tac cta	576
Thr Val Asn Asp Asn Ala Arg Cys Ile Pro Ile Phe Pro Arg Tyr Leu	
180 185 190	
gga aca tca atg aaa gca ttg att caa atg cta gag atc tgc att gga	624
Gly Thr Ser Met Lys Ala Leu Ile Gln Met Leu Glu Ile Cys Ile Gly	
195 200 205	
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210 215 220	
agg aca ctc atg aag atg cca aac att aaa ata tct cga ccc cta aaa	720
Arg Thr Leu Met Lys Met Pro Asn Ile Lys Ile Ser Arg Pro Leu Lys	
225 230 235 240	
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Val Leu Leu Thr Val Val Ile Val Phe Ile Val Thr Gln Leu Pro Tyr	
245 250 255	
aac att gtc aag ttc tgc cga gcc ata gac atc atc tac tcc ctg atc	816
Asn Ile Val Lys Phe Cys Arg Ala Ile Asp Ile Ile Tyr Ser Leu Ile	
260 265 270	

acc agc tgc aac atg agc aaa cgc atg gac atc gcc atc caa gtc aca 864
Thr Ser Cys Asn Met Ser Lys Arg Met Asp Ile Ala Ile Gln Val Thr
275 280 285

gaa agc atc gca ctc ttt cac agc tgc ctc aac cca atc ctt tat gtt 912
Glu Ser Ile Ala Leu Phe His Ser Cys Leu Asn Pro Ile Leu Tyr Val
290 295 300

ttt atg gga gca tct ttc aaa aac tac gtt atg aaa gtg gcc aag aaa 960
Phe Met Gly Ala Ser Phe Lys Asn Tyr Val Met Lys Val Ala Lys Lys
305 310 315 320

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Tyr Gly Ser Trp Arg Arg Gln Arg Gln Ser Val Glu Glu Phe Pro Phe
325 330 335

gat tct gag ggt cct aca gag cca acc agt act ttt agc att taa 1053
Asp Ser Glu Gly Pro Thr Glu Pro Thr Ser Thr Phe Ser Ile
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aacatctgcc ttattctgaa aaaaaaaaaa aaam 1147

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<213> Homo sapiens

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35 40 45
Thr Ile Val Phe Val Ile Gly Leu Ala Gly Asn Ser Met Val Val Ala
50 55 60
Ile Tyr Ala Tyr Tyr Lys Lys Gln Arg Thr Lys Thr Asp Val Tyr Ile
65 70 75 80
Leu Asn Leu Ala Val Ala Asp Leu Leu Leu Leu Phe Thr Leu Pro Phe
85 90 95
Trp Ala Val Asn Ala Val His Gly Trp Val Leu Gly Lys Ile Met Cys
100 105 110
Lys Ile Thr Ser Ala Leu Tyr Thr Leu Asn Phe Val Ser Gly Met Gln
115 120 125
Phe Leu Ala Cys Ile Ser Ile Asp Arg Tyr Val Ala Val Thr Lys Val
130 135 140
Pro Ser Gln Ser Gly Val Gly Lys Pro Cys Trp Ile Ile Cys Phe Cys
145 150 155 160
Val Trp Met Ala Ala Ile Leu Leu Ser Ile Pro Gln Leu Val Phe Tyr
165 170 175
Thr Val Asn Asp Asn Ala Arg Cys Ile Pro Ile Phe Pro Arg Tyr Leu
180 185 190
Gly Thr Ser Met Lys Ala Leu Ile Gln Met Leu Glu Ile Cys Ile Gly
195 200 205

Phe	Val	Val	Pro	Phe	Leu	Ile	Met	Gly	Val	Cys	Tyr	Phe	Ile	Thr	Ala
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Asn	Ile	Val	Lys	Phe	Cys	Arg	Ala	Ile	Asp	Ile	Ile	Tyr	Ser	Leu	Ile
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Thr	Ser	Cys	Asn	Met	Ser	Lys	Arg	Met	Asp	Ile	Ala	Ile	Gln	Val	Thr
		275					280					285			
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	290					295					300				
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305					310					315					320
Tyr	Gly	Ser	Trp	Arg	Arg	Gln	Arg	Gln	Ser	Val	Glu	Glu	Phe	Pro	Phe
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<211> 1147

<212> DNA

<213> Homo sapiens

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<223> chemokine receptor CCX CKR (variant)

<400> 3

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aaagttttcc cccctgtatt cctcacaata gttttcgtca ttggacttgc aggcaattcc 180
atggtagtgg caatttatgc ctattacaag aaacagagaa ccaaaacaga tgtgtacatc 240
ctgaatttgg ctgtagcaga tttactcctt ctattcactc tgcctttttg ggctgttaat 300
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19

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 35 40 45
 His Phe Leu Pro Pro Leu Tyr Trp Leu Val Phe Ile Val Gly Ala Leu
 50 55 60
 Gly Asn Ser Leu Val Ile Leu Val Tyr Trp Tyr Cys Thr Arg Val Lys
 65 70 75 80
 Thr Met Thr Asp Met Phe Leu Leu Asn Leu Ala Ile Ala Asp Leu Leu
 85 90 95
 Phe Leu Val Thr Leu Pro Phe Trp Ala Ile Ala Ala Asp Gln Trp
 100 105 110
 Lys Phe Gln Thr Phe Met Cys Lys Val Val Asn Ser Met Tyr Lys Met
 115 120 125
 Asn Phe Tyr Ser Cys Val Leu Leu Ile Met Cys Ile Ser Val Asp Arg
 130 135 140
 Tyr Ile Ala Ile Ala Gln Ala Met Arg Ala His Thr Trp Arg Glu Lys
 145 150 155 160
 Arg Leu Leu Tyr Ser Lys Met Val Cys Phe Thr Ile Trp Val Leu Ala
 165 170 175
 Ala Ala Leu Cys Ile Pro Glu Ile Leu Tyr Ser Gln Ile Lys Glu Glu
 180 185 190
 Ser Gly Ile Ala Ile Cys Thr Met Val Tyr Pro Ser Asp Glu Ser Thr
 195 200 205
 Lys Leu Lys Ser Ala Val Leu Thr Leu Lys Val Ile Leu Gly Phe Phe
 210 215 220
 Leu Pro Phe Val Val Met Ala Cys Cys Tyr Thr Ile Ile Ile His Thr
 225 230 235 240
 Leu Ile Gln Ala Lys Lys Ser Ser Lys His Lys Ala Leu Lys Val Thr
 245 250 255
 Ile Thr Val Leu Thr Val Phe Val Leu Ser Gln Phe Pro Tyr Asn Cys
 260 265 270
 Ile Leu Leu Val Gln Thr Ile Asp Ala Tyr Ala Met Phe Ile Ser Asn
 275 280 285
 Cys Ala Val Ser Thr Asn Ile Asp Ile Cys Phe Gln Val Thr Gln Thr
 290 295 300
 Ile Ala Phe Phe His Ser Cys Leu Asn Pro Val Leu Tyr Val Phe Val
 305 310 315 320

Gly Glu Arg Phe Arg Arg Asp Leu Val Lys Thr Leu Lys Asn Leu Gly
 325 330 335
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 <213> Homo sapiens

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 35 40 45
 Ser Lys Lys Asp Val Arg Asn Phe Lys Ala Trp Phe Leu Pro Ile Met
 50 55 60
 Tyr Ser Ile Ile Cys Phe Val Gly Leu Leu Gly Asn Gly Leu Val Val
 65 70 75 80
 Leu Thr Tyr Ile Tyr Phe Lys Arg Leu Lys Thr Met Thr Asp Thr Tyr
 85 90 95
 Leu Leu Asn Leu Ala Val Ala Asp Ile Leu Phe Leu Leu Thr Leu Pro
 100 105 110
 Phe Trp Ala Tyr Ser Ala Ala Lys Ser Trp Val Phe Gly Val His Phe
 115 120 125
 Cys Lys Leu Ile Phe Ala Ile Tyr Lys Met Ser Phe Phe Ser Gly Met
 130 135 140
 Leu Leu Leu Leu Cys Ile Ser Ile Asp Arg Tyr Val Ala Ile Val Gln
 145 150 155 160
 Ala Val Ser Ala His Arg His Arg Ala Arg Val Leu Leu Ile Ser Lys
 165 170 175
 Leu Ser Cys Val Gly Ser Ala Ile Leu Ala Thr Val Leu Ser Ile Pro
 180 185 190
 Glu Leu Leu Tyr Ser Asp Leu Gln Arg Ser Ser Ser Glu Gln Ala Met
 195 200 205
 Arg Cys Ser Leu Ile Thr Glu His Val Glu Ala Phe Ile Thr Ile Gln
 210 215 220
 Val Ala Gln Met Val Ile Gly Phe Leu Val Pro Leu Leu Ala Met Ser
 225 230 235 240
 Phe Cys Tyr Leu Val Ile Ile Arg Thr Leu Leu Gln Ala Arg Asn Phe
 245 250 255
 Glu Arg Asn Lys Ala Ile Lys Val Ile Ala Val Val Val Val Phe
 260 265 270
 Ile Val Phe Gln Leu Pro Tyr Asn Gly Val Val Leu Ala Gln Thr Val
 275 280 285
 Ala Asn Phe Asn Ile Thr Ser Ser Thr Cys Glu Leu Ser Lys Gln Leu
 290 295 300
 Asn Ile Ala Tyr Asp Val Thr Tyr Ser Leu Ala Cys Val Arg Cys Cys
 305 310 315 320
 Val Asn Pro Phe Leu Tyr Ala Phe Ile Gly Val Lys Phe Arg Asn Asp
 325 330 335

Ile	Phe	Lys	Leu	Phe	Lys	Asp	Leu	Gly	Cys	Leu	Ser	Gln	Glu	Gln	Leu
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Arg	Gln	Trp	Ser	Ser	Cys	Arg	His	Ile	Arg	Arg	Ser	Ser	Met	Ser	Val
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		35					40					45			
Val	Pro	Ile	Ala	Tyr	Ser	Leu	Ile	Cys	Val	Phe	Gly	Leu	Leu	Gly	Asn
	50					55					60				
Ile	Leu	Val	Val	Ile	Thr	Phe	Ala	Phe	Tyr	Lys	Lys	Ala	Arg	Ser	Met
65				70						75					80
Thr	Asp	Val	Tyr	Leu	Leu	Asn	Met	Ala	Ile	Ala	Asp	Ile	Leu	Phe	Val
				85					90					95	
Leu	Thr	Leu	Pro	Phe	Trp	Ala	Val	Ser	His	Ala	Thr	Gly	Ala	Trp	Val
			100					105					110		
Phe	Ser	Asn	Ala	Thr	Cys	Lys	Leu	Lys	Gly	Ile	Tyr	Ala	Ile	Asn	
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	130					135					140				
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Leu	Pro	Arg	Thr	Lys	Ile	Ile	Cys	Leu	Val	Val	Trp	Gly	Leu	Ser	Val
				165					170					175	
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		180						185					190		
Gly	Ser	Asp	Val	Cys	Glu	Pro	Lys	Tyr	Gln	Thr	Val	Ser	Glu	Pro	Ile
		195					200					205			
Arg	Trp	Lys	Leu	Leu	Met	Leu	Gly	Leu	Glu	Leu	Leu	Phe	Gly	Phe	Phe
	210					215						220			
Ile	Pro	Leu	Met	Phe	Met	Ile	Phe	Cys	Tyr	Thr	Phe	Ile	Val	Lys	Thr
225				230						235					240
Leu	Val	Gln	Ala	Gln	Asn	Ser	Lys	Arg	His	Lys	Ala	Ile	Arg	Val	Ile
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		260						265					270		
Val	Leu	Leu	Val	Thr	Ala	Ala	Asn	Leu	Gly	Lys	Met	Asn	Arg	Ser	Cys
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Gln	Ser	Glu	Lys	Leu	Ile	Gly	Tyr	Thr	Lys	Thr	Val	Thr	Glu	Val	Leu
	290					295					300				
Ala	Phe	Leu	His	Cys	Cys	Leu	Asn	Pro	Val	Leu	Tyr	Ala	Phe	Ile	Gly
305				310						315					320
Gln	Lys	Phe	Arg	Asn	Tyr	Phe	Leu	Lys	Ile	Leu	Lys	Asp	Leu	Trp	Cys
				325					330					335	
Val	Arg	Arg	Lys	Tyr	Lys	Ser	Ser	Gly	Phe	Ser	Cys	Ala	Gly	Arg	Tyr
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 Ala Ser Ser Phe Thr Met
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 <213> Homo sapiens

<220>
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 35 40 45
 Asn Ser Leu Val Leu Val Ile Ser Ile Phe Tyr His Lys Leu Gln Ser
 50 55 60
 Leu Thr Asp Val Phe Leu Val Asn Leu Pro Leu Ala Asp Leu Val Phe
 65 70 75 80
 Val Cys Thr Leu Pro Phe Trp Ala Tyr Ala Gly Ile His Glu Trp Val
 85 90 95
 Phe Gly Gln Val Met Cys Lys Ser Leu Leu Gly Ile Tyr Thr Ile Asn
 100 105 110
 Phe Tyr Thr Ser Met Leu Ile Leu Thr Cys Ile Thr Val Asp Arg Phe
 115 120 125
 Ile Val Val Val Lys Ala Thr Lys Ala Tyr Asn Gln Gln Ala Lys Arg
 130 135 140
 Met Thr Trp Gly Lys Val Thr Ser Leu Leu Ile Trp Val Ile Ser Leu
 145 150 155 160
 Leu Val Ser Leu Pro Gln Ile Ile Tyr Gly Asn Val Phe Asn Leu Asp
 165 170 175
 Lys Leu Ile Cys Gly Tyr His Asp Glu Ala Ile Ser Thr Val Val Leu
 180 185 190
 Ala Thr Gln Met Thr Leu Gly Phe Phe Leu Pro Leu Leu Thr Met Ile
 195 200 205
 Val Cys Tyr Ser Val Ile Ile Lys Thr Leu Leu His Ala Gly Gly Phe
 210 215 220
 Gln Lys His Arg Ser Leu Lys Ile Ile Phe Leu Val Met Ala Val Phe
 225 230 235 240
 Leu Leu Thr Gln Met Pro Phe Asn Leu Met Lys Phe Ile Arg Ser Thr
 245 250 255
 His Trp Glu Tyr Tyr Ala Met Thr Ser Phe His Tyr Thr Ile Met Val
 260 265 270
 Thr Glu Ala Ile Ala Tyr Leu Arg Ala Cys Leu Asn Pro Val Leu Tyr
 275 280 285
 Ala Phe Val Ser Leu Lys Phe Arg Lys Asn Phe Trp Lys Leu Val Lys
 290 295 300
 Asp Ile Gly Cys Leu Pro Tyr Leu Gly Val Ser His Gln Trp Lys Ser
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<211> 740
<212> DNA
<213> Homo sapiens

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of the GCX CKR gene

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aaataaacca agtaatttgc tattttcgtt tttattcaat ttgttgtaga tatactttta 180
cgattcacaa aattatgtat gtaaagatta taacactatt tattcttttt agttaaatac 240
taattaaatt ttcataattt aaaaatcatt tttacataaa agtccttact tttatttagg 300
atttaaatgat taagaaaatt ctccagggca ttatgtttat tgtcctgttc aaatccaagc 360
tctttcacac agaattgtac aagcaaagtt tgagtaacta atcttggggg catattccaa 420
tgtggctccc attaaagcat ttcaaagagt gctagattca ggctcacata tgttacagca 480
acaggctata ctctagggaa agaacaaaac agcttgatag aaactgtgtg cttttaagca 540
tatttagaca aatatctatc ctgtattctc tttgccatct agattggagc catggctttg 600
gaacagaacc gtcaacagat tattattatg aggagaagtg aaatgaatgg cctgatgact 660
acagtcagta tgaactgatc tgttcagaga agagacagag gatatgcaca gggttgctcc 720
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<210> 11
<211> 347
<212> DNA
<213> Homo sapiens

<220>
<223> positions 1-347 of CXC CKR

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aaagttttcc tccctgtatt cctcacata gttttcgtca ttggacttgc aggcaattcc 180
atggtagtgg caatttatgc ctattacaag aaacagagaa ccaaaacaga tgtgtacatc 240
ctgaatttgg ctgtagcaga tttactcctt ctattcactc tgcctttttg ggctgttaat 300
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<210> 12
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:peptide
translation of non-coding region of SEQ ID NO:1

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Asn Cys Ser Ala Phe Cys Leu Asp Thr Tyr Glu
1 5 10

<210> 13
<211> 5
<212> PRT
<213> Artificial Sequence

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<223> Description of Artificial Sequence:peptide
translation of non-coding region of SEQ ID NO:1

<400> 13

Cys Phe Pro Leu Lys
1 5

<210> 14

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:peptide
translation of non-coding region of SEQ ID NO:1

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Asn Ile Cys Leu Ile Leu Lys Lys Lys Lys
1 5 10